



SEQUENCE LISTING

- <110> Genentech, Inc.
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- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350
<141> 2000-09-18
- <150> PCT/US00/04414
<151> 2000-02-22
- <150> US 60/143,048
<151> 1999-07-07
- <150> US 60/145,698
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- <150> US 60/146,222
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- <150> PCT/US99/20594
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- <150> PCT/US99/20944
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<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35                      40                      45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50                      55                      60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
      65                      70                      75                      80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85                      90                      95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100                      105                      110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115                      120                      125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
      130                      135                      140

```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
305 310 315 320

Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
325 330 335

Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

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aacagccctg gctgaggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180
ggtgcggcac gaggagtttt cccggcagcg aggagtcct gagcagcatg gcccgaggga 240


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<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

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```

```

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
      20              25              30

```

```

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
  35              40              45

```

```

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
  50              55              60

```

```

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln						
	85			90		95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly						
	100		105		110	
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro						
	115		120		125	
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln						
	130		135		140	
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu						
	145		150		155	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr						
	165		170		175	
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys						
	180		185		190	
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His						
	195		200		205	
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys						
	210		215		220	
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn						
	225		230		235	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys						
	245		250		255	
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln						
	260		265		270	
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys						
	275		280		285	
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu						
	290		295		300	
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys						
	305		310		315	320
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His						
	325		330		335	
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala						
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Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
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<210> 5
<211> 45
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 5
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<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<400> 7
taagtccggc acattacagg tc                22
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<210> 8
<211> 49
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 8
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<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 9
 aaagacgcat ctgcgagtgt cc 22

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 10
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<210> 11
 <211> 2197
 <212> DNA
 <213> Homo sapiens

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tgttttaaaa taaaaccaa gtattgataa aaaaaaa 2197

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<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

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Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Pro Leu Ala Gly
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His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35             40             45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50             55             60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65             70             75             80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85             90             95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100            105            110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115            120            125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130            135            140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
      145            150            155            160

His Asp Pro Gly

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<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

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 <223> a, t, c or g

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 <222> (80)
 <223> a, t, c or g

<220>
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 <223> a, t, c or g

<220>
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 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (188)
 <223> a, t, c or g

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<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 14

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24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 15

ggcgggtatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 16

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50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
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<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 19

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24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<211> 205

<212> PRT

<213> Homo sapiens

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 Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
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 Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
 50 55 60
 Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80
 Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95
 Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
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 Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
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 Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
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 Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
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<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 24

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<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 25
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<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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 <212> DNA
 <213> Homo sapiens

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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
      35                      40                      45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
      50                      55                      60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
      65                      70                      75                      80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
      85                      90                      95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
      100                      105                      110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
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Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
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 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
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 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
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 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29

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21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu	
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Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile	
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His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu	
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Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln	
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Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His	

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Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser	260	265	270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His	275	280	285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln	290	295	300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala	305	310	315
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val	325	330	335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu	340	345	350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn	355	360	365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr	370	375	380
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys	385	390	395
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu	405	410	415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe	420	425	430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu	435	440	445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser	450	455	460
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys	465	470	475
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu	485	490	495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu	500	505	510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815
 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830
 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845
 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860
 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880
 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895
 Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910
 Arg Tyr Arg
 915

<210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35
 gtgaccctgg ttgtgaatac tcc

23

<210> 36
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36
 acagccatgg tctatagctt gg

22

<210> 37
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

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tttgatgaa aaa 1813

```

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	20	25	30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val	35	40	45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln	50	55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys	65	70	75
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro	85	90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg	100	105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val	115	120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr	130	135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu	145	150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser	165	170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro	180	185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser	195	200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys	210	215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu	225	230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly	245	250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His	260	265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp	275	280	285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380

Gln Ala Gly Ser Leu Val
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 40

agggtctcca ggagaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 42
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50

 <210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 43
 gtgtgacaca gcgtgggc 18

 <210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 44
 gaccggcagg cttctgcg 18

 <210> 45
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 45
 cagcagcttc agccaccagg agtgg 25

 <210> 46
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 46
 ctgagccgtg ggctgcagtc tcgc 24

 <210> 47

<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 47
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

<400> 48
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 gtgaaatcgc caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
 ctaattgcac taacacagaa ggaagtattt attgtatgtg tgtacctggc ttcagatcca 300
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
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```

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agacttctgt ttgctaaatc tgtttctttt tctaattatc taaaaaaaaa aaaaagggtt 2760
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aa

```

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

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Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
  1                      5                      10                      15

```

```

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
          20                      25                      30

```

```

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
          35                      40                      45

```

```

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
          50                      55                      60

```

```

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
          65                      70                      75                      80

```

```

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
          85                      90                      95

```

```

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
          100                      105                      110

```

```

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
          115                      120                      125

```

```

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
          130                      135                      140

```

```

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
          145                      150                      155                      160

```

```

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
          165                      170                      175

```

```

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

180							185							190						
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val					
		195					200				205									
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys					
		210			215						220									
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe					
225				230						235				240						
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys					
				245				250						255						
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met					
		260						265						270						
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Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser					
		290				295						300								
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln					
305				310						315				320						
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile					
				325				330						335						
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys					
		340						345				350								
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser					
		355				360						365								
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp					
370						375				380										
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser					
385				390						395				400						
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly					
				405				410						415						
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln					
		420						425				430								
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr					
		435				440						445								
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys					
450						455				460										

```

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
465                               470                               475                               480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
                               485                               490                               495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
                               500                               505                               510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
                               515                               520                               525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
                               530                               535                               540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545                               550                               555                               560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
                               565                               570                               575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
                               580                               585                               590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
                               595                               600                               605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
                               610                               615                               620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625                               630                               635                               640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
                               645                               650                               655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
                               660                               665                               670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
                               675                               680                               685

Leu Arg
690

<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (61)

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<223> a, t, c or g

<400> 50

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tggaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaatggca atgttgagcag tgcattttta tattataaga 120
gtattggtcc ctttgctttc atcatctgac aacttcctat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
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gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
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aatcacctga cacattttgc aattttgatg tcctctggtc cttccattgg tattaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta ttctactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 51

```

ggtaatgagc tccattacag 20

```

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 52

```

ggagtagaaa ggcgatgg 18

```

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 53

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cacctgatac catgaatggc ag 22

```

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 57

atgagacca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

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gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

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Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205
 Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61

gcctcccggc ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 62
 ccagtccggt gacaagccca aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
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 gctgctgctg cgctacctgg tggtcgccct gggctatcat aaggcctatg ggttttctgc 180
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggtatatt tagcctgcaa 240
 aacccccaaag aagactgttt cctccagatt agagtggaag aaactgggtc ggagtgtctc 300
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 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaaagtatt 480
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<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
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 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300
 Gly Gly Ser Arg Gly Gln Glu Phe

305 310

<210> 65
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 65
 atcggtgtga agttagtgcc cc 22

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 66
 acctgcgata tccaacagaa ttg 23

<210> 67
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 67
 ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 68
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 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
 aaataaatga attactcaat ctccatgac catctataca tactccacct tcaaaaagta 240
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 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtac 540

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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
      20             25             30

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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
      35             40             45

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Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
      50             55             60

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Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65 70 75 80
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190
 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255
 Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285
 Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300
 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320
 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

	340		345		350										
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn
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Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
	370					375					380				
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro
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Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405					410					415	
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
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Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
	435						440					445			
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	450					455						460			
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
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Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
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	515						520					525			
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545					550					555					560
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
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Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys
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	595						600					605			
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	610					615					620				

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
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<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
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<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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```

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Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
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Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
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 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
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 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
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 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
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 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
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 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525
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 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560
 Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590	
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser			
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Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile			
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<210> 74			
<211> 22			
<212> DNA			
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<220>			
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tcacctggag cctttattgg cc			22
<210> 75			
<211> 23			
<212> DNA			
<213> Artificial Sequence			
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 75			
ataccageta taaccaggct gcg			23
<210> 76			
<211> 52			
<212> DNA			
<213> Artificial Sequence			
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			
<400> 76			
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg			50
gg			52
<210> 77			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe			

<400> 77
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<210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 78
 gggaatagat gtgatctgat tgg 23

<210> 79
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 79
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<210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 80
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<210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 81
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<210> 82

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 82
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<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
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 agccagggag ccggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180
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<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

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			20					25					30		
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu
		35					40					45			
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn
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Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp
65					70					75					80
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser
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Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile
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Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly
		115					120					125			
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu
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Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala
145					150					155					160
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro
				165					170					175	
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser
			180					185					190		
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val
		195					200					205			
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser
	210					215					220				
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp
225					230					235					240
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly
				245					250					255	
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser
			260					265					270		
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe
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Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
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Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
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Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87
 cctagcacag tgacgaggga cttggc 26

<210> 88
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 88
 aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 89
 gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
 <211> 2755
 <212> DNA
 <213> Homo sapiens

<400> 90
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
  1                      5                      10                     15

```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
      20                      25                     30

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```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
      35                      40                     45

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```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
      50                      55                     60

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```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
      65                      70                     75                     80

```

```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
      85                      90                     95

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Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
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 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
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 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
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 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
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 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
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 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
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 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
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 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn
 405 410 415
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
 420 425 430
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
 435 440 445
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro
 450 455 460
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
 465 470 475 480
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
 485 490 495
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
 500 505 510
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
 530 535 540
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
 595 600 605
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
 610 615 620
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
 625 630 635 640
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

660	665	670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp		
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Cys Gly Ser His Ser Leu Ser Asp		
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<210> 92
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 92
 gttgatctg ggcaacaata ac 22

<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 93
 attgttgtagc aggctgagtt taag 24

<210> 94
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 94
 ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95
 <211> 2226
 <212> DNA
 <213> Homo sapiens

<400> 95
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 tggcgcgtgg gcccgcgggg ggattcttgg cagttggggg gtccgctcggg agcgagggcg 180

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gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
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gttgat 2226

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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

```

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
  1                      5                      10                      15

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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
          20                      25                      30

```

```

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
          35                      40                      45

```

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Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
          50                      55                      60

```

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
 100 105 110
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97

tggaaggaga tgcatgccca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 99
 acagagcaga gggcgccttg 20

 <210> 100
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 100
 tcagggacaa gtggtgtctc tccc 24

 <210> 101
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 101
 tcaggggaagg agtgtgcagt tctg 24

 <210> 102
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 102
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50

 <210> 103
 <211> 2026
 <212> DNA
 <213> Homo sapiens

<400> 103

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cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctcctca ggggaaacta 60
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tatcccccg gctacctggc cgcgccgcgg cgggtgcgcg gtgagagggg gcgcgcgggc 180
agccgagcgc cgggtgtgagc cagcgtgctg gccagtgtga gcggcggtgt gagegcgggtg 240
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gctgccatga ggggcgcgaa cgcctggggg cactctgcc tgctgctggc tgccgccacc 360
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ggagagtctg gatttattgg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttgga aaatcacagt tcccgaagga aaagtagtgc ttctcaattt ccgattcata 540
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gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
          20                      25                      30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
          35                      40                      45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
          50                      55                      60

```

Val	Pro	Glu	Gly	Lys	Val	Val	Val	Leu	Asn	Phe	Arg	Phe	Ile	Asp	Leu	
65					70					75					80	
Glu	Ser	Asp	Asn	Leu	Cys	Arg	Tyr	Asp	Phe	Val	Asp	Val	Tyr	Asn	Gly	
				85					90					95		
His	Ala	Asn	Gly	Gln	Arg	Ile	Gly	Arg	Phe	Cys	Gly	Thr	Phe	Arg	Pro	
			100					105					110			
Gly	Ala	Leu	Val	Ser	Ser	Gly	Asn	Lys	Met	Met	Val	Gln	Met	Ile	Ser	
		115					120					125				
Asp	Ala	Asn	Thr	Ala	Gly	Asn	Gly	Phe	Met	Ala	Met	Phe	Ser	Ala	Ala	
		130				135					140					
Glu	Pro	Asn	Glu	Arg	Gly	Asp	Gln	Tyr	Cys	Gly	Gly	Leu	Leu	Asp	Arg	
145					150					155					160	
Pro	Ser	Gly	Ser	Phe	Lys	Thr	Pro	Asn	Trp	Pro	Asp	Arg	Asp	Tyr	Pro	
				165					170					175		
Ala	Gly	Val	Thr	Cys	Val	Trp	His	Ile	Val	Ala	Pro	Lys	Asn	Gln	Leu	
			180					185					190			
Ile	Glu	Leu	Lys	Phe	Glu	Lys	Phe	Asp	Val	Glu	Arg	Asp	Asn	Tyr	Cys	
		195					200					205				
Arg	Tyr	Asp	Tyr	Val	Ala	Val	Phe	Asn	Gly	Gly	Glu	Val	Asn	Asp	Ala	
	210					215					220					
Arg	Arg	Ile	Gly	Lys	Tyr	Cys	Gly	Asp	Ser	Pro	Pro	Ala	Pro	Ile	Val	
225					230					235					240	
Ser	Glu	Arg	Asn	Glu	Leu	Leu	Ile	Gln	Phe	Leu	Ser	Asp	Leu	Ser	Leu	
				245					250					255		
Thr	Ala	Asp	Gly	Phe	Ile	Gly	His	Tyr	Ile	Phe	Arg	Pro	Lys	Lys	Leu	
			260					265					270			
Pro	Thr	Thr	Thr	Glu	Gln	Pro	Val	Thr	Thr	Thr	Phe	Pro	Val	Thr	Thr	
		275					280					285				
Gly	Leu	Lys	Pro	Thr	Val	Ala	Leu	Cys	Gln	Gln	Lys	Cys	Arg	Arg	Thr	
	290					295					300					
Gly	Thr	Leu	Glu	Gly	Asn	Tyr	Cys	Ser	Ser	Asp	Phe	Val	Leu	Ala	Gly	
305					310					315					320	
Thr	Val	Ile	Thr	Thr	Ile	Thr	Arg	Asp	Gly	Ser	Leu	His	Ala	Thr	Val	
				325					330					335		
Ser	Ile	Ile	Asn	Ile	Tyr	Lys	Glu	Gly	Asn	Leu	Ala	Ile	Gln	Gln	Ala	

	340		345		350										
Gly	Lys	Asn	Met	Ser	Ala	Arg	Leu	Thr	Val	Val	Cys	Lys	Gln	Cys	Pro
	355						360					365			
Leu	Leu	Arg	Arg	Gly	Leu	Asn	Tyr	Ile	Ile	Met	Gly	Gln	Val	Gly	Glu
	370					375					380				
Asp	Gly	Arg	Gly	Lys	Ile	Met	Pro	Asn	Ser	Phe	Ile	Met	Met	Phe	Lys
385					390					395					400
Thr	Lys	Asn	Gln	Lys	Leu	Leu	Asp	Ala	Leu	Lys	Asn	Lys	Gln	Cys	
			405						410					415	

<210> 105
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 105
 ccgattcata gacctcgaga gt 22

<210> 106
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 106
 gtcaaggagt cctccacaat ac 22

<210> 107
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 107
 gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

<210> 108
 <211> 1838
 <212> DNA

<213> Homo sapiens

<400> 108

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aagggcctag tcccagctgt gctctggggc ctgagcctct tcttcaacct cccaggacct 180
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tgttcaccac atccccacac ccatttgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
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Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20              25              30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35              40              45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50              55              60

```

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
 65 70 75 80
 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
 85 90 95
 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
 100 105 110
 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
 115 120 125
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
 130 135 140
 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
 145 150 155 160
 Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
 165 170 175
 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
 180 185 190
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
 195 200 205
 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
 210 215 220
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
 225 230 235 240
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
 245 250 255
 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
 260 265 270
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
 275 280 285
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
 290 295 300
 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
 305 310 315 320
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
 325 330 335
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctogatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgcctcttgc tcctccaggg 60
 cagcaccatg cagccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcaccccca cccacgtgag 240
 ggcccagtac gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagaggtt 300
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360
 gctggtgttc ggcattggagc agcggctgcc gcccaacagc gagctggtgc aggcctgtgt 420
 gcggctcttc caggagccgg tccccaaagg cgcgctgcac aggcacgggc ggctgtcccc 480
 gcgcagcgcc cggggccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540
 ccgcacctcc ctcactgact ccaggctggg gtccgtccac gagagcggct ggaaggcctt 600
 cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgtgtgt 660
 gctacagggt tcggtgcaga gggagcatct gggcccgcgt gcgtccggcg cccacaagct 720
 ggtccgcttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780
 caccctggac cttggggact atggagctca gggcgactgt gaccctgaag caccaatgac 840
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 cgagaactgg gtgctggagc ccccggtctt cctggcttat gagtgtgtgg gcacctgccg 960
 gcagcccccg gaggccctgg ccttcaagtg gccgtttctg gggcctcgac agtgcacgc 1020
 ctcgagact gactcgctgc ccattgatcg cagcatcaag gagggaggca ggaccaggcc 1080
 ccagggtgtc agcctgccc acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140
 gtcctgcca aggaggctcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200
 gtgtgtgttt ctgaagtgtt cgagggtacc aggagagctg gcgatgactg aactgtgtat 1260
 ggacaaatgc tctgtgctct ctagttagcc ctgaatttgc ttctctgac aagtacctc 1320
 acctaathtt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380
 ttctctatct ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440
 acctgagggc agaaagccc ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500
 aaagtctcc accaccactc tggacctaa acctggggtt aagtgtgggt tgtgcatccc 1560
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1 5 10 15
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 115

aggactgccca taacttgccct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggtgtgt tgtgtcagtgc gcttgatcgc gatggggaca 60
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tctgagaat 180

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aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240
tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tctgtcttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tcccctgtca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaattgctg tgcgcatgga agctgtggag cggaatgtgg gggatcatcg ggcagccgtc 780
cttgaacccc tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840
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gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc ccctacttct 1080
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
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agggatcagg aaggaatcct ggggatgcca ttgacttccc ttctaagtag acagcaaaaa 1260
tgccgggggt cgcaggaatc tgcactcaac tgcccactg gctggcaggg atctttgaat 1320
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tctagagcgg gaattagagg ctagagcggc tgaaatgggt gtttgggtgat gacactgggg 1440
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agctcttggt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggatttaaa 1620
accgctgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcggg tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tggatcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

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<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

```

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1                      5                      10                      15

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```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
          20                      25                      30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
          35                      40                      45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
          50                      55                      60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
          65                      70                      75                      80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
          85                      90                      95

```

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
 245 250 255
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 121
 tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

 <210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 122
 acacctgggtt caaagatggg 20

 <210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 123
 taggaagagt tgctgaaggc acgg 24

 <210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 124
 ttgccttact caggtgctac 20

 <210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125

actcagcagt ggtaggaaag

20

<210> 126

<211> 1210

<212> DNA

<213> Homo sapiens

<400> 126

```

cagcgcgtgg cggcgccgc tgtggggaca gcatgagcgg cggttggatg gcgcagggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgtgctgct gctgctcggc ctgggactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc ccctgccccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgctt agcaggcgag ctccgttgca cgtgagcga tgactgcatt ccactcacgt 480
ggcgctgcga cggccacca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaaggg gatgccacaa ccattggggc ccctgtgacc ctggagagtg 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gacctggag agtgtccccct 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaaagcca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctccctcttt 780
tgtcctggct ccgagcccag gagcgctcc gccactggg gttactggtg gccatgaagg 840
agtcctctgt gctgtcagaa cagaagacct cgtgcctctg aggacaagca cttgccacca 900
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
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agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200
aagttgcttc
1210

```

<210> 127

<211> 282

<212> PRT

<213> Homo sapiens

<400> 127

```

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
  1             5             10             15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
    20             25             30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
    35             40             45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
    50             55             60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
    65             70             75             80

```

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129
 ttggttccac agccgagctc gtcg 24

<210> 130
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 130
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131
 <211> 1843
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1837)
 <223> a, t, c or g

<400> 131
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 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccca 180
 gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
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 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
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 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
 gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactc 540
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
 atgaaggatt caagatccgg tacccecgacc tacacaatat ggtttcatta tgcgcgatg 660
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
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 agcaaactg gcccagcacc catgagaccc tcctgaccac gtggaagatt gtggcggttca 1140


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cggcaaccag tgtgtctgtg gtgtctgtgc tcgtcatcct ggccaggatg ttccagacca 1200
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gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

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<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

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Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
 1             5             10             15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
      20             25             30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
      35             40             45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
      50             55             60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
      65             70             75             80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
      85             90             95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
      100             105             110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
      115             120             125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
      130             135             140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
      145             150             155             160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
      165             170             175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

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180							185					190				
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr	
		195					200					205				
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys	
	210					215					220					
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu	
225					230					235					240	
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe	
				245					250					255		
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val	
			260					265					270			
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr	
		275					280					285				
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys	
	290					295					300					
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr	
305					310					315					320	
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu	
				325					330					335		
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His	
			340					345					350			
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe	
		355					360					365				
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala	
	370					375					380					
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val	
385					390					395					400	
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr	
			405					410						415		
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys	
			420				425						430			
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro	
		435					440					445				
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile	
	450					455					460					

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttacia aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cggtccgtcg gtggcctaga 60
 gatgctgctg ccgcggttgc agttgtgcgc cagccctctg cccgccagcc cgctccaccg 120
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgccctgc 240
 tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300

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ggccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcgga 600
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gagaggtcgc cttgaatctg gcctacatcc taatccccag cattccccct ctcctcctcc 900
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aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

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<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<210> 138

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140
 cagtccaagc ataaaggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120
 ttgtgtttgc ctctgcagc ctcaaccgcg agggcagcga gggcctacca ccatgatcac 180
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgactcg 240
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600
 tgtggaagac attccctttc ttccaccaac cttcaaccca caggaggtct ttattcgttc 660
 cactaacatt tttcggaatc tggagtccac ccgttggttg ctggctgggc ttttccagtg 720

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tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
tttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900
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cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaacaga gagctgtgga 1020
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attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgcccccca 1140
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ttaccagcac ctggaatcta aggagtgggt tgtgcagctc tattaccacg ggaaggagca 1320
ggtgcogaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380
agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaactc aggtgatgga 1440
agttggaaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500
gcctttatac aatg 1514

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<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

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Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
 1             5             10             15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
      20             25             30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
      35             40             45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
      50             55             60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
      65             70             75             80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
      85             90             95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
      100            105            110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
      115            120            125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
      130            135            140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
      145            150            155            160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
      165            170            175

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Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agtcatcac ctacacctgc cttgggtcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

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gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtgatgac ggctgggaca ttaaggacgt ggctgtgttg tgccgggagc tgggctgttg 300
agctgccagc ggaacccta gtggtathtt gtatgagcca ccagcagaaa aagagcaaaa 360
ggcctccatc caatcagtc gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480
gagctctttc tccccagtc cagagggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccgggcc gcaaagggtg tgtccggca gctgggatgt gggagggtg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720
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caaccatgat gaagacacgt gggtcgaatg tgaagatccc ttgacttga gactagtagg 840
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acggaattht aaggataaat thttctgaatt ggttatgggg thttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

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<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgcacctcg 60
 acccacgcgt ccgcggacgc gtgggcccgc gcgtgggccc gctaccagga agagtctgcc 120
 gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
 cctgggcgctc ttccggcctct tccggetgct gcagtgggtg cgcgggaagg cctacctgcg 240
 gaatgctgtg gtggtgatca caggcggcac ctccagggtg ggcaaagaat gtgcaaaagt 300
 cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
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 tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
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 ggtggcccag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
 cttactgcct tccttggtctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

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gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc caggggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
cttggccgcc atggccaac ttgtttattg cagcttataa tgggttac 1427

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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1               5               10               15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
      20               25               30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
      35               40               45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
      50               55               60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
      65               70               75               80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
      85               90               95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
      100              105              110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
      115              120              125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
      130              135              140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
      145              150              155              160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
      165              170              175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
      180              185              190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
      195              200              205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

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210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235 240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
	245	250 255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
	260	265 270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
	275	280 285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
	290	300

Arg Lys Ser Lys Asn Ser
305 310

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154
gggtgctaaac tgggtgctctg tggc

24

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155
cagggcaaga tgagcattcc

20

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156
tcataactggt ccattctcggc acgc 24

```
<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 157
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

```
<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens
```

<400> 158						
ccccacgcgtc	cgctggtgtt	agatcgagca	accctctaaa	agcagtttag	agtggtaaaa	60
aaaaaaaaaaa	acacacccaaa	cgctcgcagc	cacaaaaggg	atgaaatttc	ttctggacat	120
cctcctgctt	ctcccgttac	tgatcgtctg	ctccctagag	tccttcgtga	agctttttat	180
tcctaagagg	agaaaaatcag	tcaccggcga	aatcgtgctg	attacaggag	ctgggcatgg	240
aattggggaga	ctgactgcct	atgaatttgc	taaacttaaa	agcaagctgg	ttctctggga	300
tataaataag	catggactgg	aggaaacagc	tgccaaatgc	aagggactgg	gtgccaaagt	360
tcataccttt	gtggtagact	gcagcaaccg	agaagatat	tacagctctg	caaagaaggt	420
gaaggcagaa	attggagatg	ttgatttttt	agtaataaat	gctggtgtag	ctctatacat	480
agatttgttt	gtcacaacaag	atcctcagat	tgaaaagact	tttgaagtta	atgtacttgc	540
acattttctgg	actacaaagg	catttcttcc	tgcaatgacg	aagaataacc	atggccatat	600
tgtcactgtg	gcttcggcag	ctggacatgt	ctcggtcctc	ttcttactgg	cttactgttc	660
aagcaagttt	gctgctgttg	gatttccata	aactttgaca	gatgaactgg	ctgccttaca	720
aataactgga	gtcaaaacaa	catgtctgtg	tcctaatttc	gtaaacactg	gcttcaccaa	780
aaatccaagt	acaagtttgg	gaccactct	ggaacctgag	gaagtggtaa	acaggctgat	840
gcatgggatt	ctgactgagc	agaagatgat	ttttattcca	tcttctatag	cttttttaac	900
aacattggaa	aggatccttc	ctgagcgttt	cctggcagtt	ttaaaacgaa	aatcagtggt	960
taagtttgat	gcagttattg	gatataaaaa	gaaagcgcaa	taagcaccta	gtttttcgaa	1020
aacctgattta	ccaggttttag	gttgatgtca	tctaatagtg	ccagaatttt	aatgtttgaa	1080
cttctgtttt	ttctaattat	ccccatttct	tcaatatcat	ttttgaggct	ttggcagctc	1140
tcattttacta	ccacttgttc	tttagccaaa	agctgattac	atatgatata	aacagagaaa	1200
taccttttaga	ggtgacttta	aggaaaatga	agaaaaagaa	ccaaaatgac	tttattaaaa	1260
taattttccaa	gattattttgt	ggctcacctg	aaggtcttgc	aaaatttgta	ccataaccgt	1320
ttattttaaca	tatattttta	tttttgattg	cacttaaatt	ttgtataatt	tgtgtttctt	1380
tttctgttct	acataaaatc	agaaacttca	agctctctaa	ataaaatgaa	ggactatata	1440
tagtggtatt	tcacaatgaa	tatcatgaac	tctcaatggg	taggtttcat	cctaccatt	1500
gccactctgt	ttcctgagag	atacctcaca	ttccaatgcc	aaacatttct	gcacagggaa	1560
gctagagggtg	gatacacgtg	ttgcaagtat	aaaagcatca	ctgggattta	aggagaattg	1620
agagaaatgta	cccacaaatg	gcagcaataa	taaattggatc	acacttaaaa	aaaaaaaaaaa	1680
aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	1740
aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	a			1771

<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

```

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
 1           5           10           15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
      20           25           30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
      35           40           45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
      50           55           60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
      65           70           75           80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
      85           90           95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
      100          105          110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
      115          120          125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
      130          135          140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
      145          150          155          160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
      165          170          175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
      180          185          190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
      195          200          205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
      210          215          220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
      225          230          235          240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
      245          250          255

```


Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

```
<210> 160
<211> 23
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

```
<400> 160
ggatgaaggca gaaattggag atg                23
```

```
<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 161
atcccatgca tcagcctgtt tacc 24

```
<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 162
gctgggtgtag tctatacatc agatttgttt gctacacaag atcctcag 48

```
<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens
```

<400> 163
 cccacgcgtc cgcggaacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
 tcagggagga gcaccgactg cggcgcaccc tgagagatgg ttggtgccat gtggaaggtg 120

```

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
agaagtgttt ccatgccacc taaggagagc tcaggacagc cattatttct caccctttac 240
attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360
ttctttctggt tcttcccagc tcagatacag ccagaagatg ccccagtagt tctctggcta 420
caggggtgggc cgggaggttc atccatgttt ggactctttg tggaacatgg gccttatgtt 480
gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660
atatctcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
tatgcagaat tctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900
aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggcctttgaa 960
atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatggt 1020
acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080
tatgtgaaat ttttgtcact cccagaggtg agacaagcca tccacgtggg gaatcagact 1140
tttaatgatg gaactatagt tgaaaagtac ttgcgagaag atacagtaca gtcagttaag 1200
ccatgggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260
atcatcgtgg cagctgccct gacagagcgc tcttctgatg gcattggactg gaaaggatcc 1320
caggaataca agaaggcaga aaaaaaagtt tggaagatct ttaaacttga cagtgaagtg 1380
gctgggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440
attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500
aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560
cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620
tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740
ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800
ttttaggggtc ttgaatagga agttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860
taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920
gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

```

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

```

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
  1             5             10            15

```

```

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
      20             25            30

```

```

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
      35             40            45

```

```

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
      50             55            60

```

```

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

```

65		70		75		80
Asn Lys Thr Tyr	Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln					
	85		90			95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro						
	100		105			110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val						
	115		120			125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr						
	130		135			140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser						
	145		150		155	160
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala						
		165		170		175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu						
	180		185			190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys						
	195		200			205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg						
	210		215			220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser						
	225		230		235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile						
		245		250		255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His						
	260		265			270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu						
	275		280			285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr						
	290		295			300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys						
	305		310		315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro						
		325		330		335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly						
	340		345			350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgccca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167

agctctcaga ggctggtcat aggg

24

<210> 168

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 169

```

cgagggcctt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
atccccccct ttccctaaca gttctaacag ctgttctaac agctagtgat caggggttct 120
tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
tccttgccct tctgtggata acagagcatg agaaagtga gagatgcagc ggagtgaggt 240
gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gacgattga 300
cctggagagg ctgggggagg gctgcctaa caagctttca aaaaacagga gcgacttcca 360
ctgggctggg ataagacgtg ccggtaggat agggagact gggtttagtc ctaatatcaa 420
attgactggc tgggtgaact tcaacagcct ttaacctct ctgggagatg aaaacgatgg 480
cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540
tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccgaaa ttatttttgg 720
tctgaccact ctgccttgtg ttttgagaaa tcatgtgagg gccaacggg gaaggtggag 780
cagatgagca cacacaggag ccgtctctc accgccgcc ctctcagcat ggaacagagg 840
cagccctggc cccgggccct ggaggtggac agccgctctg tggctctgct ctgagtggtc 900
tgggtgctgc tggccccccc agcagccggc atgctcagt tcagcacctt ccactctgag 960
aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020
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acagggccag aagaggacaa caagtctcgt taccgcccc tcactgtgca gccctgcagc 1140
gaagtgtca cctcaccaa caatgtcaac aagctgtca tcattgacta ctctgagaac 1200
cgctgtctgg cctgtgggag cctctaccag ggggtctgca agctgtctgc gctggatgac 1260
ctcttcaccc tgggtggagg atcccacaag aaggagcact acctgtccag tgtcaacaag 1320
acgggcacca tgtacggggg gattgtgcgc tctgaggggt aggatggcaa gctcttcac 1380
ggcacggctg tggatgggaa gcaggattac ttcccagccc tgtccagccg gaagctgccc 1440
cgagaccctg agtcctcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500
ctcatcaaga tcccttcaga caccctggcc ctgggtctccc actttgacat cttctacatc 1560
tacggctttg ctagtggggg ctttgtctac tttctcactg tccagcccga gaccctgag 1620
ggtgtggcca tcaactccgc tggagacctc ttctacacct cacgcacgtg gcggctctgc 1680

```

```

aaggatgacc ccaagttcca ctcatacgtg tccctgccct tgggctgcac ccgggcccggg 1740
gtggaatacc gcctcctgca ggctgcttac ctggccaagc ctggggactc actggcccag 1800
gccttcaata tcaccagcca ggacgatgta ctctttgccca tcttctccaa agggcagaag 1860
cagtatcacc acccgcccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920
ttgcagatca aggagcgctt gcagtcctgc taccagggcg agggcaacct ggagctcaac 1980
tggctgctgg ggaaggacgt ccagtgcacg aaggcgccctg tccccatcga tgataacttc 2040
tgtggactgg acatcaacca gcccctggga ggctcaactc cagtggaggg cctgaccctg 2100
tacaccacca gcagggaccg catgacctct gtggcctcct acgtttacaa cggtacagc 2160
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agatttaact ataggcaact ttattttctt ggggaacaaa ggtgaaatgg ggaggtaaga 2340
aggggttaat tttgtgactt agcttctagc tacttctctc agccatcagt cattgggtat 2400
gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460
acatctgcaa aagcaaa 2477

```

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

```

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
  1              5              10              15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
      20              25              30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35              40              45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
      50              55              60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
      65              70              75              80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
      85              90              95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
      100             105             110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115             120             125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130             135             140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145             150             155             160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
      165             170             175

```

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450 455 460
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
 465 470 475 480
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
 485 490 495
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
 500 505 510
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
 515 520 525
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
 530 535 540
 Leu Tyr Phe Leu Gly Glu Gln Arg
 545 550

<210> 171
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 171
 tggaataaccg cctcctgcag 20

<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 172
 cttctgccct ttggagaaga tggc 24

<210> 173
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 173
ggactcactg gcccaggcct tcaatatcac cagccaggac gat

42

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1683)
<223> a, t, c or g

<400> 174
aggctcccgc gcgcggctga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag 60
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120
tgctggctcgt cttgggcttc ctgggtgctc gcaggtcga ctggagcacc ctggctccctc 180
tgcggtccg ccacgcacag ctggggctgc aggccaaagg ctggaacttc atgctggagg 240
attccacctt ctggatcttc gggggctcca tccactatct ccgtgtgccc agggagtact 300
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360
cgtggaacct gcctgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccct 480
acatctgcag tgagatggac ctccggggct tgcccagctg gctactccaa gacctggca 540
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tgatgtccag ggtggtgcca ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

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Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1                      5                      10          15

```

```

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
      20                      25          30

```

```

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
      35                      40          45

```

```

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
      50                      55          60

```

```

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
      65                      70          75          80

```

```

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
      85                      90          95

```

```

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
      100                     105          110

```

```

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
      115                     120          125

```

```

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
      130                     135          140

```

Leu	Gly	Gly	Leu	Pro	Ser	Trp	Leu	Leu	Gln	Asp	Pro	Gly	Met	Arg	Leu	145	150	155	160
Arg	Thr	Thr	Tyr	Lys	Gly	Phe	Thr	Glu	Ala	Val	Asp	Leu	Tyr	Phe	Asp	165	170	175	
His	Leu	Met	Ser	Arg	Val	Val	Pro	Leu	Gln	Tyr	Lys	Arg	Gly	Gly	Pro	180	185	190	
Ile	Ile	Ala	Val	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Asn	Lys	Asp	195	200	205	
Pro	Ala	Tyr	Met	Pro	Tyr	Val	Lys	Lys	Ala	Leu	Glu	Asp	Arg	Gly	Ile	210	215	220	
Val	Glu	Leu	Leu	Leu	Thr	Ser	Asp	Asn	Lys	Asp	Gly	Leu	Ser	Lys	Gly	225	230	235	240
Ile	Val	Gln	Gly	Val	Leu	Ala	Thr	Ile	Asn	Leu	Gln	Ser	Thr	His	Glu	245	250	255	
Leu	Gln	Leu	Leu	Thr	Thr	Phe	Leu	Phe	Asn	Val	Gln	Gly	Thr	Gln	Pro	260	265	270	
Lys	Met	Val	Met	Glu	Tyr	Trp	Thr	Gly	Trp	Phe	Asp	Ser	Trp	Gly	Gly	275	280	285	
Pro	His	Asn	Ile	Leu	Asp	Ser	Ser	Glu	Val	Leu	Lys	Thr	Val	Ser	Ala	290	295	300	
Ile	Val	Asp	Ala	Gly	Ser	Ser	Ile	Asn	Leu	Tyr	Met	Phe	His	Gly	Gly	305	310	315	320
Thr	Asn	Phe	Gly	Phe	Met	Asn	Gly	Ala	Met	His	Phe	His	Asp	Tyr	Lys	325	330	335	
Ser	Asp	Val	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Val	Leu	Thr	Glu	Ala	Gly	340	345	350	
Asp	Tyr	Thr	Ala	Lys	Tyr	Met	Lys	Leu	Arg	Asp	Phe	Phe	Gly	Ser	Ile	355	360	365	
Ser	Gly	Ile	Pro	Leu	Pro	Pro	Pro	Pro	Asp	Leu	Leu	Pro	Lys	Met	Pro	370	375	380	
Tyr	Glu	Pro	Leu	Thr	Pro	Val	Leu	Tyr	Leu	Ser	Leu	Trp	Asp	Ala	Leu	385	390	395	400
Lys	Tyr	Leu	Gly	Glu	Pro	Ile	Lys	Ser	Glu	Lys	Pro	Ile	Asn	Met	Glu	405	410	415	
Asn	Leu	Pro	Val	Asn	Gly	Gly	Asn	Gly	Gln	Ser	Phe	Gly	Tyr	Ile	Leu	420	425	430	

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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aaggggagca aagccgggct cggcccagg cccccaggac ctccatctcc caatgttgga 180
ggaatccgac acgtgacggg ctgtccgccc tctcagacta gaggagcgt gtaaaccgca 240
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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

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Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
  1              5              10              15

```

```

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
          20              25              30

```

```

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
      35              40              45

```

```

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
      50              55              60

```

Asp	Arg	Leu	Leu	Lys	Met	Arg	Trp	Ser	Gly	Leu	Asn	Ala	Ile	Gln	Phe	65	70	75	80
Tyr	Val	Pro	Trp	Asn	Tyr	His	Glu	Pro	Gln	Pro	Gly	Val	Tyr	Asn	Phe	85	90	95	
Asn	Gly	Ser	Arg	Asp	Leu	Ile	Ala	Phe	Leu	Asn	Glu	Ala	Ala	Leu	Ala	100	105	110	
Asn	Leu	Leu	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ala	Glu	Trp	115	120	125	
Glu	Met	Gly	Gly	Leu	Pro	Ser	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Ile	His	130	135	140	
Leu	Arg	Thr	Ser	Asp	Pro	Asp	Phe	Leu	Ala	Ala	Val	Asp	Ser	Trp	Phe	145	150	155	160
Lys	Val	Leu	Leu	Pro	Lys	Ile	Tyr	Pro	Trp	Leu	Tyr	His	Asn	Gly	Gly	165	170	175	
Asn	Ile	Ile	Ser	Ile	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala	180	185	190	
Cys	Asp	Phe	Ser	Tyr	Met	Arg	His	Leu	Ala	Gly	Leu	Phe	Arg	Ala	Leu	195	200	205	
Leu	Gly	Glu	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Asp	Gly	Pro	Glu	Gly	Leu	210	215	220	
Lys	Cys	Gly	Ser	Leu	Arg	Gly	Leu	Tyr	Thr	Thr	Val	Asp	Phe	Gly	Pro	225	230	235	240
Ala	Asp	Asn	Met	Thr	Lys	Ile	Phe	Thr	Leu	Leu	Arg	Lys	Tyr	Glu	Pro	245	250	255	
His	Gly	Pro	Leu	Val	Asn	Ser	Glu	Tyr	Tyr	Thr	Gly	Trp	Leu	Asp	Tyr	260	265	270	
Trp	Gly	Gln	Asn	His	Ser	Thr	Arg	Ser	Val	Ser	Ala	Val	Thr	Lys	Gly	275	280	285	
Leu	Glu	Asn	Met	Leu	Lys	Leu	Gly	Ala	Ser	Val	Asn	Met	Tyr	Met	Phe	290	295	300	
His	Gly	Gly	Thr	Asn	Phe	Gly	Tyr	Trp	Asn	Gly	Ala	Asp	Lys	Lys	Gly	305	310	315	320
Arg	Phe	Leu	Pro	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Ser	325	330	335	
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile				

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
	405	410
		415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
	420	425
		430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
	435	440
		445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
	450	455
		460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
		480
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
	485	490
		495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
	500	505
		510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
	515	520
		525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
	530	535
		540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
		560
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
	565	570
		575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
	580	585
		590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
	595	600
		605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
	610	615
		620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 182
 tggcacccag aatggtgttg gctc 24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 183
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc 50

<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
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<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

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Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
  1             5             10             15

```

```

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
      20             25             30

```

```

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
      35             40             45

```

```

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
      50             55             60

```

```

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
      65             70             75             80

```

```

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
      85             90             95

```

```

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
      100            105            110

```

```

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
      115            120            125

```

```

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
      130            135            140

```

```

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
      145            150            155            160

```

```

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
      165            170            175

```

```

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
      180            185            190

```

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465 470 475 480
 Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
 485 490 495
 Phe Ala Asn Gly Ile
 500

<210> 186
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 186
 cctccctcta ttacccatgt c 21

<210> 187
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 187
 gaccaacttt ctctgggagt gagg 24

<210> 188
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 188
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag 47

<210> 189
 <211> 2917
 <212> DNA
 <213> Homo sapiens

<400> 189
 cccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60
 acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccttggg 120
 aagacatttg tgttttacac acataaggat ctgtgtttgg ggtttcttct tcctccctg 180

```

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300
atcgctgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360
ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420
cacaacccag acaaggtgtg gtgggccaag aacagccagg ccaaaacccat tgccacggag 480
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gaagatgatg taatacaaag tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160
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tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880
ggcctgaaag tgacacacag gccctgcatgt aaaaaaa 2917

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<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met	Glu	Leu	Val	Arg	Arg	Leu	Met	Pro	Leu	Thr	Leu	Leu	Ile	Leu	Ser	1	5	10	15
Cys	Leu	Ala	Glu	Leu	Thr	Met	Ala	Glu	Ala	Glu	Gly	Asn	Ala	Ser	Cys	20	25	30	
Thr	Val	Ser	Leu	Gly	Gly	Ala	Asn	Met	Ala	Glu	Thr	His	Lys	Ala	Met	35	40	45	
Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg	50	55	60	
Pro	Glu	Asn	Lys	Ser	Ile	Arg	Ile	Ile	Phe	Ser	Tyr	Val	Gln	Leu	Asp	65	70	75	80
Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr	85	90	95	
Ser	Ser	Asn	Gly	Pro	Leu	Leu	Gly	Gln	Val	Cys	Ser	Lys	Asn	Asp	Tyr	100	105	110	
Val	Pro	Val	Phe	Glu	Ser	Ser	Ser	Ser	Thr	Leu	Thr	Phe	Gln	Ile	Val	115	120	125	
Thr	Asp	Ser	Ala	Arg	Ile	Gln	Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe	130	135	140	
Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr	145	150	155	160
Leu	Glu	Gly	Ser	Phe	Thr	Ser	Pro	Asn	Tyr	Pro	Lys	Pro	His	Pro	Glu	165	170	175	
Leu	Ala	Tyr	Cys	Val	Trp	His	Ile	Gln	Val	Glu	Lys	Asp	Tyr	Lys	Ile	180	185	190	
Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys	195	200	205	
Phe	Asp	Phe	Leu	Ala	Ile	Tyr	Asp	Gly	Pro	Ser	Thr	Asn	Ser	Gly	Leu	210	215	220	
Ile	Gly	Gln	Val	Cys	Gly	Arg	Val	Thr	Pro	Thr	Phe	Glu	Ser	Ser	Ser	225	230	235	240
Asn	Ser	Leu	Thr	Val	Val	Leu	Ser	Thr	Asp	Tyr	Ala	Asn	Ser	Tyr	Arg	245	250	255	
Gly	Phe	Ser	Ala	Ser	Tyr	Thr	Ser	Ile	Tyr	Ala	Glu	Asn	Ile	Asn	Thr	260	265	270	
Thr	Ser	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Met	Arg	Val	Ile	Ile	Ser	Lys	275	280	285	

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

	565	570	575	
Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe				
	580	585	590	
Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr				
	595	600	605	

<210> 191
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 191
 tctctattcc aaactgtggc g 21

<210> 192
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 192
 tttgatgacg attcgaaggt gg 22

<210> 193
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 193
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194
 <211> 2362
 <212> DNA
 <213> Homo sapiens

<400> 194
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60
 cgggacatgc ggccccagga gctccccagg ctcgcgttcc cgttgctgct gttgctgttg 120
 ctgctgctgc cgccgcgcgc gtgccctgcc cacagcgcca cgcgcttcga cccacactgg 180


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gagtccttgg acgcccgcga gctgcccgcg tggtttgacc aggccaagtt cggcatcttc 240
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caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattaccc tcttagtttc 360
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gagaaggtag agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgagtga tgtgaaggcc 2160
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ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
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taaactcatt gtgcaaatgt aa 2362

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<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

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Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
  1              5              10              15

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Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
              20              25              30

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Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
  35              40              45

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Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
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 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220
 Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
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Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 198
 aacttgacgc atcagccact ctgc 24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 199
 ttccgtgccc agcttcggta gcgagtgggt ctggtggtat tggca 45

<210> 200
 <211> 2372
 <212> DNA
 <213> Homo sapiens

<400> 200
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 catctgaggt gtttccctgg ctctgaaggg gtaggcacga tggccagggtg cttcagcctg 180
 gtggtgcttc tcacttccat ctggaccacg aggtcctctg tccaaggctc tttgcgtgca 240
 gaagagcttt ccatccagggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300
 gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360
 ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
 ggctgggttg gagatggatt cgtgggtcatc tctaggatta gcccaaacc caagtgtggg 480
 aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540
 tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660
 acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tctcctgct 720
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780
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 aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900
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 gtccataata tatcccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
 1             5             10             15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
      20             25             30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
      35             40             45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
      50             55             60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
      65             70             75             80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
      85             90             95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
      100            105            110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
      115            120            125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
      130            135            140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 203
 gtcagtgcaca gtacctactc gg 22

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 204
 tggagcagga ggagtagtag tagg 24

<210> 205
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 205
 aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206
 <211> 1620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (973)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (977)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (996)
 <223> a, t, c or g

<220>
 <221> modified_base

<222> (1003)

<223> a, t, c or g

<400> 206

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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

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Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
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Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20             25             30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 35             40             45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50             55             60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65             70             75             80

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Arg	Arg	Ser	Ile	Thr	Val	Glu	Gln	His	Ile	Gly	Asn	Ile	Phe	Met	Phe	
					85					90					95	
Ser	Lys	Val	Ala	Asn	Thr	Ile	Leu	Phe	Phe	Arg	Leu	Asp	Ile	Arg	Met	
			100					105					110			
Gly	Leu	Leu	Tyr	Ile	Thr	Leu	Cys	Ile	Val	Phe	Leu	Met	Thr	Cys	Lys	
			115				120					125				
Pro	Pro	Leu	Tyr	Met	Gly	Pro	Glu	Tyr	Ile	Lys	Tyr	Phe	Asn	Asp	Lys	
	130					135					140					
Thr	Ile	Asp	Glu	Glu	Leu	Glu	Arg	Asp	Lys	Arg	Val	Thr	Trp	Ile	Val	
145					150					155					160	
Glu	Phe	Phe	Ala	Asn	Trp	Ser	Asn	Asp	Cys	Gln	Ser	Phe	Ala	Pro	Ile	
				165					170					175		
Tyr	Ala	Asp	Leu	Ser	Leu	Lys	Tyr	Asn	Cys	Thr	Gly	Leu	Asn	Phe	Gly	
			180					185					190			
Lys	Val	Asp	Val	Gly	Arg	Tyr	Thr	Asp	Val	Ser	Thr	Arg	Tyr	Lys	Val	
		195					200					205				
Ser	Thr	Ser	Pro	Leu	Thr	Lys	Gln	Leu	Pro	Thr	Leu	Ile	Leu	Phe	Gln	
	210					215					220					
Gly	Gly	Lys	Glu	Ala	Met	Arg	Arg	Pro	Gln	Ile	Asp	Lys	Lys	Gly	Arg	
225					230					235					240	
Ala	Val	Ser	Trp	Thr	Phe	Ser	Glu	Glu	Asn	Val	Ile	Arg	Glu	Phe	Asn	
				245					250					255		
Leu	Asn	Glu	Leu	Tyr	Gln	Arg	Ala	Lys	Lys	Leu	Ser	Lys	Ala	Gly	Asp	
			260					265					270			
Asn	Ile	Pro	Glu	Glu	Gln	Pro	Val	Ala	Ser	Thr	Pro	Thr	Thr	Val	Ser	
		275					280					285				
Asp	Gly	Glu	Asn	Lys	Lys	Asp	Lys									
	290					295										
<210> 208																
<211> 24																
<212> DNA																
<213> Artificial Sequence																
<220>																
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe																
<400> 208																
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<210> 209

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 209

tggagacaat atccctgagg

20

<210> 210

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 210

aacagttggc cacagcatgg cagg

24

<210> 211

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 211

ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag

50

<210> 212

<211> 1985

<212> DNA

<213> Homo sapiens

<400> 212

ggacagctcg cggccccga gagctctagc cgctcgaggag ctgcctgggg acgtttgccc 60
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caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240
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aaaaaa                                           1985

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<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

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Met Gly Leu Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
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Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
                20                      25          30
Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
    35                      40          45
Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
    50                      55          60
Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
    65                      70          75          80
Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
                85                      90          95
Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
    100                      105          110
Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr		
130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu		
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg		
	165	170
		175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala		
	180	185
		190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly		
	195	200
		205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr		
210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro		
225	230	235
		240
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp		
	245	250
		255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu		
	260	265
		270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu		
	275	280
		285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys		
290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser		
305	310	315
		320
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu		
	325	330
		335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr		
	340	345
		350
Gly Val Tyr Cys Tyr Arg Gln His		
355	360	

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214
tgcttcgcta ctgccctc 18

<210> 215
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215
ttcccttgtag ggttgag 18

<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216
agggtggaa gccagttc 18

<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217
agccagttag gaaatgcg 18

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218
tgtccaaagt acacacacct gagg 24

<210> 219
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 219
 gatgccacga tgcgcaaggt gggacagctc tttgccgcct ggaag 45

<210> 220
 <211> 1503
 <212> DNA
 <213> Homo sapiens

<400> 220
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 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaa 1503

<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens

<400> 226
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<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

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Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
      35           40           45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
      50           55           60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
      65           70           75           80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
      85           90           95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
      100          105          110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
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Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
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Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
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Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
      165          170          175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
      180          185          190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
      195          200          205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
      210          215          220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
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Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
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 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
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 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
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 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
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 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
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 435 440 445
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 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
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 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495
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<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228
tggtctcgca caccgatc 18

<210> 229
<211> 18
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<220>
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oligonucleotide probe

<400> 229
ctgctgtcca caggggag 18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatagcaa tttccgcc 18

<210> 232

<211> 18
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 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232

ttcctcaaga gggcagcc

18

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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<400> 233

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24

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

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45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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          20              25              30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
          35              40              45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
          50              55              60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
          65              70              75             80

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Glu	Thr	Asn	Thr	Asp	Thr	Lys	Val	Gly	Asn	Asn	Thr	Ile	His	Val	His	
			100					105					110			
Arg	Glu	Ile	His	Lys	Ile	Thr	Asn	Asn	Gln	Thr	Gly	Gln	Met	Val	Phe	
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Ser	Glu	Thr	Val	Ile	Thr	Ser	Val	Gly	Asp	Glu	Glu	Gly	Arg	Arg	Ser	
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Leu	Glu	Asp	Leu	Glu	Arg	Ser	Leu	Thr	Glu	Glu	Met	Ala	Leu	Gly	Glu	
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Pro	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Gly	Gly	Glu	Glu	Ile			
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<210> 237

<211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 237
 ggagctgcac cccttgc 17

 <210> 238
 <211> 49
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 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 238
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 <210> 239
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 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 239
 gcagagcgga gatgcagcgg cttg 24

 <210> 240
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 <400> 240
 ttggcagctt catggagg 18

 <210> 241
 <211> 18
 <212> DNA
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 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 241
 cctgggcaaa aatgcaac 18

<210> 242
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 <212> DNA
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<220>
 <223> Synthetic Oligonucleotide Probe

<400> 242
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24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
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45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

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 ggcattccga agctgacttt ctataggcaa tttgtacct ttgtggagaa 3600
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 aataaaaaata aataataaca ataaaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met	Arg	Leu	Leu	Val	Ala	Pro	Leu	Leu	Leu	Ala	Trp	Val	Ala	Gly	1	5	10	15
Ala	Thr	Ala	Thr	Val	Pro	Val	Val	Pro	Trp	His	Val	Pro	Cys	Pro	20	25	30	
Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser	35	40	45	
Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu	50	55	60	
Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu	65	70	75	
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly	80	85	90	
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe	95	100	105	
Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu	110	115	120	
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His	125	130	135	
Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His	140	145	150	

Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	155	160	165
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	170	175	180
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	185	190	195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	200	205	210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	215	220	225
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	230	235	240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	245	250	255
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	260	265	270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	275	280	285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	290	295	300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	305	310	315
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	320	325	330
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	335	340	345
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	350	355	360
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	365	370	375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	380	385	390
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	395	400	405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys			

	410		415		420
Leu Pro Leu Ile	Ser Pro Arg Ser Phe	Pro Pro Ser Leu Gln Val			
	425		430		435
Ala Ser Gly Glu	Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu			
	440		445		450
Pro Glu Pro Glu	Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu			
	455		460		465
Thr Pro Ala His	Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly			
	470		475		480
Thr Leu Glu Leu	Arg Arg Val Thr Ala	Glu Glu Ala Gly Leu Tyr			
	485		490		495
Thr Cys Val Ala	Gln Asn Leu Val Gly	Ala Asp Thr Lys Thr Val			
	500		505		510
Ser Val Val Val	Gly Arg Ala Leu Leu	Gln Pro Gly Arg Asp Glu			
	515		520		525
Gly Gln Gly Leu	Glu Leu Arg Val Gln	Glu Thr His Pro Tyr His			
	530		535		540
Ile Leu Leu Ser	Trp Val Thr Pro Pro	Asn Thr Val Ser Thr Asn			
	545		550		555
Leu Thr Trp Ser	Ser Ala Ser Ser Leu	Arg Gly Gln Gly Ala Thr			
	560		565		570
Ala Leu Ala Arg	Leu Pro Arg Gly Thr	His Ser Tyr Asn Ile Thr			
	575		580		585
Arg Leu Leu Gln	Ala Thr Glu Tyr Trp	Ala Cys Leu Gln Val Ala			
	590		595		600
Phe Ala Asp Ala	His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr			
	605		610		615
Lys Glu Ala Thr	Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly			
	620		625		630
Leu Ile Ala Ile	Leu Ala Leu Ala Val	Leu Leu Leu Ala Ala Gly			
	635		640		645
Leu Ala Ala His	Leu Gly Thr Gly Gln	Pro Arg Lys Gly Val Gly			
	650		655		660
Gly Arg Arg Pro	Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser			
	665		670		675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
 680 685 690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
 695 700 705

Leu Pro Pro Leu Ser Gln Asn Ser
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<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgcatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgatcg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaagccaag ggcgtgtttg agaaggtgaa gaagttccgg acccatgtgg 50

aggaggggga cattgtgtac cgcctctaca tgcggcagac catcatcaag 100

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catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200
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cacactgtgg tggatgctac ggcgtccct caagaagtac tcgtttgagt 350
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 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met	Arg	Gln	Thr	Ile	Ile	Lys	Val	Ile	Lys	Phe	Ile	Leu	Ile	Ile
1				5					10				15	
Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp
				20					25				30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg
				35					40				45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe
				50					55				60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr
				65					70				75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu
				80					85				90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys

	95		100		105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro	110		115		120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu	125		130		135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp	140		145		150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu	155		160		165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp	170		175		180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val	185		190		195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu	200		205		210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala	215		220		225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp	230		235		240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu	245		250		255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr	260		265		270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu	275		280		285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp	290		295		300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr	305		310		315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr	320		325		330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser	335		340		345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn	350		355		360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His	
				365					370					375	
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile	
				380					385					390	
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu	
				395					400					405	
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys	
				410					415					420	
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe	
				425					430					435	
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala	
				440					445					450	
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln	
				455					460					465	
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln	
				470					475					480	
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile	
				485					490					495	
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly	
				500					505					510	
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp	
				515					520					525	
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg	
				530					535					540	
Ala	Asp	Lys	Glu	Gln	Ala										
				545											

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50
 gcgctctccc gtcccgcggt ggttgctgct gctgccgctg ctgctgggcc 100
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
 tgggattatg tgacggtcgg caaggatgcc tacatgttct ggtggctcta 200
 ttatgccacc aactcctgca agaacttctc agaactgccc ctgggtcatgt 250
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20						25				30	

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35						40				45	

Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	50	55	60
Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	65	70	75
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	80	85	90
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	95	100	105
Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	110	115	120
Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	125	130	135
Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	140	145	150
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	155	160	165
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	170	175	180
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	185	190	195
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	200	205	210
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	215	220	225
Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	230	235	240
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	245	250	255
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	260	265	270
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	275	280	285
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	290	295	300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly			

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg
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Ala	Gly	Leu	Arg	Lys	Pro	Glu	Ser	Gln	Glu	Ala	Ala	Pro	Leu	Ser
						20						25		30

Gly	Pro	Cys	Gly	Arg	Arg	Val	Ile	Thr	Ser	Arg	Ile	Val	Gly	Gly
			35						40					45

Glu	Asp	Ala	Glu	Leu	Gly	Arg	Trp	Pro	Trp	Gln	Gly	Ser	Leu	Arg
			50						55					60

Leu	Trp	Asp	Ser	His	Val	Cys	Gly	Val	Ser	Leu	Leu	Ser	His	Arg
				65					70					75

Trp	Ala	Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Thr	Tyr	Ser	Asp	Leu
				80					85					90

Ser	Asp	Pro	Ser	Gly	Trp	Met	Val	Gln	Phe	Gly	Gln	Leu	Thr	Ser	95	100	105
Met	Pro	Ser	Phe	Trp	Ser	Leu	Gln	Ala	Tyr	Tyr	Thr	Arg	Tyr	Phe	110	115	120
Val	Ser	Asn	Ile	Tyr	Leu	Ser	Pro	Arg	Tyr	Leu	Gly	Asn	Ser	Pro	125	130	135
Tyr	Asp	Ile	Ala	Leu	Val	Lys	Leu	Ser	Ala	Pro	Val	Thr	Tyr	Thr	140	145	150
Lys	His	Ile	Gln	Pro	Ile	Cys	Leu	Gln	Ala	Ser	Thr	Phe	Glu	Phe	155	160	165
Glu	Asn	Arg	Thr	Asp	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Ile	Lys	170	175	180
Glu	Asp	Glu	Ala	Leu	Pro	Ser	Pro	His	Thr	Leu	Gln	Glu	Val	Gln	185	190	195
Val	Ala	Ile	Ile	Asn	Asn	Ser	Met	Cys	Asn	His	Leu	Phe	Leu	Lys	200	205	210
Tyr	Ser	Phe	Arg	Lys	Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly	215	220	225
Asn	Ala	Gln	Gly	Gly	Lys	Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly	230	235	240
Pro	Leu	Ala	Cys	Asn	Lys	Asn	Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	245	250	255
Val	Ser	Trp	Gly	Val	Gly	Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	260	265	270
Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu	Trp	Ile	Gln	Lys	Leu	Met	275	280	285
Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro	Ser	Trp	Pro	Leu	Leu	290	295	300
Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu	Gly	Pro	Val		305	310	

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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				20						25					30
Leu	Pro	Pro	Gly	Trp	Val	Ser	Leu	Gly	Arg	Ala	Asp	Pro	Glu	Glu	
				35					40					45	
Glu	Leu	Ser	Leu	Thr	Phe	Ala	Leu	Arg	Gln	Gln	Asn	Val	Glu	Arg	
				50					55					60	
Leu	Ser	Glu	Leu	Val	Gln	Ala	Val	Ser	Asp	Pro	Ser	Ser	Pro	Gln	
				65					70					75	
Tyr	Gly	Lys	Tyr	Leu	Thr	Leu	Glu	Asn	Val	Ala	Asp	Leu	Val	Arg	
				80					85					90	
Pro	Ser	Pro	Leu	Thr	Leu	His	Thr	Val	Gln	Lys	Trp	Leu	Leu	Ala	
				95					100					105	
Ala	Gly	Ala	Gln	Lys	Cys	His	Ser	Val	Ile	Thr	Gln	Asp	Phe	Leu	
				110					115					120	
Thr	Cys	Trp	Leu	Ser	Ile	Arg	Gln	Ala	Glu	Leu	Leu	Leu	Pro	Gly	
				125					130					135	
Ala	Glu	Phe	His	His	Tyr	Val	Gly	Gly	Pro	Thr	Glu	Thr	His	Val	
				140					145					150	
Val	Arg	Ser	Pro	His	Pro	Tyr	Gln	Leu	Pro	Gln	Ala	Leu	Ala	Pro	
				155					160					165	
His	Val	Asp	Phe	Val	Gly	Gly	Leu	His	Arg	Phe	Pro	Pro	Thr	Ser	
				170					175					180	
Ser	Leu	Arg	Gln	Arg	Pro	Glu	Pro	Gln	Val	Thr	Gly	Thr	Val	Gly	
				185					190					195	
Leu	His	Leu	Gly	Val	Thr	Pro	Ser	Val	Ile	Arg	Lys	Arg	Tyr	Asn	
				200					205					210	
Leu	Thr	Ser	Gln	Asp	Val	Gly	Ser	Gly	Thr	Ser	Asn	Asn	Ser	Gln	
				215					220					225	
Ala	Cys	Ala	Gln	Phe	Leu	Glu	Gln	Tyr	Phe	His	Asp	Ser	Asp	Leu	
				230					235					240	
Ala	Gln	Phe	Met	Arg	Leu	Phe	Gly	Gly	Asn	Phe	Ala	His	Gln	Ala	
				245					250					255	
Ser	Val	Ala	Arg	Val	Val	Gly	Gln	Gln	Gly	Arg	Gly	Arg	Ala	Gly	
				260					265					270	
Ile	Glu	Ala	Ser	Leu	Asp	Val	Gln	Tyr	Leu	Met	Ser	Ala	Gly	Ala	
				275					280					285	

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	290	295	300
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	305	310	315
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	320	325	330
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	335	340	345
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	350	355	360
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	365	370	375
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	380	385	390
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	395	400	405
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	410	415	420
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	425	430	435
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	440	445	450
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	455	460	465
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	470	475	480
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	485	490	495
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	500	505	510
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	515	520	525
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	530	535	540
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	545	550	555

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<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu	1	5	10	15
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Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	35	40	45	
Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	50	55	60	
Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	65	70	75	
Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	80	85	90	
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile	95	100	105	
Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser	110	115	120	

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp Cys Arg Glu Gly	380		

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

<400> 262
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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu	1	5	10	15
Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	20	25	30	
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
				305					310					315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
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<220>
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<400> 268
ggggaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
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<220>
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<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatgggac tccaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccggagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
gggcagggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccatata gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggcg actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tggtaggagct gcacaacctc taccggggccc 150
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt gggggccacaa 250
 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350
 tacaacctca gcgcccgcac ctgcagccca ggccagatgt gcggccacta 400
 cacgcagggtg gtatggggca agacagagag gatcggtgtt ggttcccact 450
 tctgtgagaa gctccagggt gttgaggaga ccaacatoga attactggtg 500
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 gccagggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200
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 ggccctccgg aagggaagg ctacggggca tgtgcctcat cacaccatcc 1550
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 ggactgcaca ccggggccac acctctcctg cccctccctc ctgagtctg 1650
 ggggtgggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700
 tgccacaca gcatgtgcgc tctcctgag tgctgtgta gctggggatg 1750
 gggattccta ggggcagatg aaggacaagc cccactggag tggggttctt 1800
 tgagtggggg aggcagggac gagggaagga aagtaactcc tgactctcca 1850
 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp					
			20						25					30					
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala					
			35						40					45					
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp					
			50						55					60					
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val					
			65						70					75					
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe					
			80						85					90					
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu					
			95						100					105					
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys					
			110						115					120					
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala					
			125						130					135					

Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu	140	145	150
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr	155	160	165
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly	170	175	180
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser	185	190	195
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro	200	205	210
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser	215	220	225
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile	230	235	240
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys	245	250	255
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr	260	265	270
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr	275	280	285
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu	290	295	300
Asp	Glu	Glu	Pro	Val	Thr	Phe	Pro	Lys	Ser	Thr	His	Val	Pro	Ile	305	310	315
Pro	Lys	Ser	Ala	Asp	Lys	Val	Thr	Asp	Lys	Thr	Lys	Val	Pro	Ser	320	325	330
Arg	Ser	Pro	Glu	Asn	Ser	Leu	Asp	Pro	Lys	Met	Ser	Leu	Thr	Gly	335	340	345
Ala	Arg	Glu	Leu	Leu	Pro	His	Ala	Gln	Glu	Glu	Ala	Glu	Ala	Glu	350	355	360
Ala	Glu	Leu	Pro	Pro	Ser	Ser	Glu	Val	Leu	Ala	Ser	Val	Phe	Pro	365	370	375
Ala	Gln	Asp	Lys	Pro	Gly	Glu	Leu	Gln	Ala	Thr	Leu	Asp	His	Thr	380	385	390
Gly	His	Thr	Ser	Ser	Lys	Ser	Leu	Pro	Asn	Phe	Pro	Asn	Thr	Ser	395	400	405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

tcattctcca agttatgggtg gacgtacttc tgttggttctc cctctgcttg 100
 ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150
 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200
 acaacaatga attggagacc attccaaatc tgggaccagt ctcggaat 250
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 aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750
 gcaggaactt catctcagcc aaaatgcat caacaggatc agccctgatg 800
 cctgggagtt ctgccagaag ctgagtgcg tggacctaac tttcaatcac 850
 ttatcaaggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900
 actgcacatt gggacaaca gagtgcgcta cattgctgat tgtgccttcc 950
 gggggctttc cagtttaaag actttggatc tgaagaaca tgaaatttcc 1000
 tggactattg aagacatgaa tgggtgctttc tctgggcttg acaaactgag 1050
 gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100
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 gcatttaaat acatcaagcc ttttgtgoga ttgccagcta aaatggctcc 1250
 cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300
 gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400
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 agattttcag gaagaaaadc acatttgtac ctttaaacag actttagaaa 3200
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<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20					25				30	

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser	50	55	60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu	65	70	75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu	80	85	90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro	95	100	105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met	185	190	195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn	230	235	240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu	245	250	255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser	260	265	270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser			

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Leu Lys Thr Leu	Asp 305	Leu Lys Asn Asn	Glu 310	Ile Ser Trp Thr	Ile 315
Glu Asp Met Asn	Gly 320	Ala Phe Ser Gly	Leu 325	Asp Lys Leu Arg	Arg 330
Leu Ile Leu Gln	Gly 335	Asn Arg Ile Arg	Ser 340	Ile Thr Lys Lys	Ala 345
Phe Thr Gly Leu	Asp 350	Ala Leu Glu His	Leu 355	Asp Leu Ser Asp	Asn 360
Ala Ile Met Ser	Leu 365	Gln Gly Asn Ala	Phe 370	Ser Gln Met Lys	Lys 375
Leu Gln Gln Leu	His 380	Leu Asn Thr Ser	Ser 385	Leu Leu Cys Asp	Cys 390
Gln Leu Lys Trp	Leu 395	Pro Gln Trp Val	Ala 400	Glu Asn Asn Phe	Gln 405
Ser Phe Val Asn	Ala 410	Ser Cys Ala His	Pro 415	Gln Leu Leu Lys	Gly 420
Arg Ser Ile Phe	Ala 425	Val Ser Pro Asp	Gly 430	Phe Val Cys Asp	Asp 435
Phe Pro Lys Pro	Gln 440	Ile Thr Val Gln	Pro 445	Glu Thr Gln Ser	Ala 450
Ile Lys Gly Ser	Asn 455	Leu Ser Phe Ile	Cys 460	Ser Ala Ala Ser	Ser 465
Ser Asp Ser Pro	Met 470	Thr Phe Ala Trp	Lys 475	Lys Asp Asn Glu	Leu 480
Leu His Asp Ala	Glu 485	Met Glu Asn Tyr	Ala 490	His Leu Arg Ala	Gln 495
Gly Gly Glu Val	Met 500	Glu Tyr Thr Thr	Ile 505	Leu Arg Leu Arg	Glu 510
Val Glu Phe Ala	Ser 515	Glu Gly Lys Tyr	Gln 520	Cys Val Ile Ser	Asn 525
His Phe Gly Ser	Ser 530	Tyr Ser Val Lys	Ala 535	Lys Leu Thr Val	Asn 540
Met Leu Pro Ser	Phe 545	Thr Lys Thr Pro	Met 550	Asp Leu Thr Ile	Arg 555

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Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
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Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
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Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
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Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
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Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
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Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
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Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
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Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
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Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
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Thr Gly Cys Ser	Pro Asp Pro Arg Thr Val	Leu Met Asp His Tyr
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Glu Pro Ser Tyr	Ile Lys Lys Lys Glu Cys	Tyr Pro Cys Ser His
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Pro Ser Glu Glu	Ser Cys Glu Arg Ser Phe	Ser Asn Ile Ser Trp
920	925	930
Pro Ser His Val	Arg Lys Leu Leu Asn Thr	Ser Tyr Ser His Asn
935	940	945
Glu Gly Pro Gly	Met Lys Asn Leu Cys Leu	Asn Lys Ser Ser Leu
950	955	960
Asp Phe Ser Ala	Asn Pro Glu Pro Ala Ser	Val Ala Ser Ser Asn
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Ser Phe Met Gly	Thr Phe Gly Lys Ala Leu	Arg Arg Pro His Leu
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Asp Ala Tyr Ser	Ser Phe Gly Gln Pro Ser	Asp Cys Gln Pro Arg
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Ala Phe Tyr Leu	Lys Ala His Ser Ser Pro	Asp Leu Asp Ser Gly
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Ser Glu Glu Asp	Gly Lys Glu Arg Thr Asp	Phe Gln Glu Glu Asn
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His Ile Cys Thr	Phe Lys Gln Thr Leu Glu	Asn Tyr Arg Thr Pro
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<210> 291

<211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
				35					40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
				50					55					60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
				65					70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
				80					85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
				95					100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
				110					115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
				125					130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
				140					145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

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Glu Leu Lys Arg Leu Ser Tyr Ile Ser	Glu Gly Ala Phe Glu Gly	
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Glu Ile Pro Asn Leu Thr Pro Leu Ile	Lys Leu Asp Glu Leu Asp	
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Leu Ser Gly Asn His Leu Ser Ala Ile	Arg Pro Gly Ser Phe Gln	
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Gly Leu Met His Leu Gln Lys Leu Trp	Met Ile Gln Ser Gln Ile	
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275	280	285
Leu Phe Thr Pro Leu His His Leu Glu	Arg Ile His Leu His His	
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Gln Asn Tyr Phe Thr Cys Tyr Ala Pro	Val Ile Val Glu Pro Pro	
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Arg Ala Ser Thr Ser Leu Thr Ser Val	Ser Trp Ile Thr Pro Asn	
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr	Lys Val Arg Ile Ala Val	
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr	Asn Val Thr Val Gln Asp	
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr	425	430	435
Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro	440	445	450
Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser	455	460	465
Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro	470	475	480
Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro	485	490	495
Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr	500	505	510
Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr	515	520	525
Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala	530	535	540
Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His	545	550	555
Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn	560	565	570
Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu	575	580	585
Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser	590	595	600
Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn	605	610	615
Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn	620	625	630
Ser Lys Asp Asn Val Gln Glu Thr Gln Ile	635	640	

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
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Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
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Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
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Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
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Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met	245		250		255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu	260		265		270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly	275		280		285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn	290		295		300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu	305		310		315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser	320		325		330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn	335		340		345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser	350		355		360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile	365		370		375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg	380		385		390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala	395		400		405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn	410		415		420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys	425		430		435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys	440		445		450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln	455		460		465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly	470		475		480

Arg Ser Ile Phe	Ala Val Ser Pro Asp	Gly Phe Val Cys Asp Asp	485	490	495
Phe Pro Lys Pro	Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser Ala	500	505	510
Ile Lys Gly Ser	Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser Ser	515	520	525
Ser Asp Ser Pro	Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu Leu	530	535	540
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala Gln	545	550	555
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg Glu	560	565	570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser Asn	575	580	585
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val Asn	590	595	600
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile Arg	605	610	615
Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His Pro	620	625	630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe Pro	635	640	645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp Val	650	655	660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr Ser	665	670	675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala Thr	680	685	690
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu Asp	695	700	705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile Ala	710	715	720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp Ser	725	730	735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn Gln	740	745	750

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	755	760	765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	770	775	780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met	785	790	795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	800	805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	815	820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	830	835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	845	850	855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	860	865	870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	875	880	885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	890	895	900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	905	910	915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	920	925	930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	935	940	945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	950	955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	965	970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	980	985	990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	995	1000	1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu			

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Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu					
	1040		1045		1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg					
	1055		1060		1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly					
	1070		1075		1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn					
	1085		1090		1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro					
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr					
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<400> 297
ggctggagac actgaacct 19

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gggtcttggt gaatgagg 18

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<223> Synthetic Oligonucleotide Probe

<400> 304

ccccatgtgt ccatgactgt tccc 24

<210> 305

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<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 305

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<210> 306

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<400> 308

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<210> 309

<211> 50

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<400> 309

gccttcactg gtttgatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310

<211> 3296

<212> DNA

<213> Homo Sapien

<400> 310

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 311

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<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 312

gcggccacgg tccttggaat tg 22

<210> 313

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 313

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<210> 314

<211> 3003

<212> DNA

<213> Homo Sapien

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aat 3003

<210> 315

<211> 509

<212> PRT

<213> Homo Sapien

<400> 315

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Ser	Ser	Ile	Gly	Leu	Cys	Arg	Tyr	Gly	Gly	Arg	Ile	Asp	Cys	Cys	35	40	45	
Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
Gln	Pro	Arg	Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	65	70	75	
Lys	Cys	His	Pro	Gly	Tyr	Ala	Gly	Lys	Thr	Cys	Asn	Gln	Asp	Leu	80	85	90	
Asn	Glu	Cys	Gly	Leu	Lys	Pro	Arg	Pro	Cys	Lys	His	Arg	Cys	Met	95	100	105	
Asn	Thr	Tyr	Gly	Ser	Tyr	Lys	Cys	Tyr	Cys	Leu	Asn	Gly	Tyr	Met	110	115	120	
Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
Ala	Asn	Cys	Gln	Tyr	Gly	Cys	Asp	Val	Val	Lys	Gly	Gln	Ile	Arg	140	145	150	
Cys	Gln	Cys	Pro	Ser	Pro	Gly	Leu	His	Leu	Ala	Pro	Asp	Gly	Arg	155	160	165	

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Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys	185	190	195
Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr	200	205	210
Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys	215	220	225
Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys	230	235	240
Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr	245	250	255
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro	260	265	270
Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn	275	280	285
Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro	290	295	300
Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr	305	310	315
Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro	320	325	330
Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr	335	340	345
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala	350	355	360
Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln	365	370	375
Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val	380	385	390
His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu	395	400	405
Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly	410	415	420
Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys			

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
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455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
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<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

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<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggacccacg tacg 24

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

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<210> 319

<211> 2110

<212> DNA

<213> Homo Sapien

<400> 319

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catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
cactccagca tcagacatcc agatcatatg gctatttgag agacccca 250
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 agacttgtga acacttaagg aaatgactat taaagtctta tttttatttt 2050
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 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

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Ala	Cys	Ser	Gly	Leu	Lys	Val	Thr	Val	Pro	Ser	His	Thr	Val	His
				20					25					30
Gly	Val	Arg	Gly	Gln	Ala	Leu	Tyr	Leu	Pro	Val	His	Tyr	Gly	Phe
				35					40					45
His	Thr	Pro	Ala	Ser	Asp	Ile	Gln	Ile	Ile	Trp	Leu	Phe	Glu	Arg
				50					55					60

Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	65	70	75
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	80	85	90
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	95	100	105
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	110	115	120
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	125	130	135
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	140	145	150
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	155	160	165
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	170	175	180
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	185	190	195
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	200	205	210
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	215	220	225
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	230	235	240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	245	250	255
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	260	265	270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	275	280	285
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	290	295	300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	305	310	315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu			

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro	Leu Ala Ser Ile Thr Gly	
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met	Cys Leu Leu Phe Leu Trp	
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile	Lys Gln Lys Leu Glu Gly	
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala	Gln Thr Phe Ser Gly His	
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile	Tyr Glu Phe Val Ala Phe	
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile	Pro Ser Arg Ser Val Pro	
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp	Leu His Ser Thr Val Tyr	
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln	Gln Gln Asp His Pro Glu	
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<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

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<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
 tggatgatag aattttatgc cccgtggtgc cctgcttgct aaaatcttca 200
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250
 ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatc 300
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 aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450
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aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

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Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
				35					40					45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210

Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu

	215		220		225									
Ser	Glu	Ser	Ala	Gln	Pro	Leu	Lys	Lys	Val	Glu	Glu	Glu	Gln	Glu
				230					235					240
Ala	Asp	Glu	Glu	Asp	Val	Ser	Glu	Glu	Glu	Ala	Glu	Ser	Lys	Glu
				245					250					255
Gly	Thr	Asn	Lys	Asp	Phe	Pro	Gln	Asn	Ala	Ile	Arg	Gln	Arg	Ser
				260					265					270
Leu	Gly	Pro	Ser	Leu	Ala	Thr	Asp	Lys	Ser					
				275					280					

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

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<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

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<210> 328

<211> 21

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 329
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<210> 330
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 <212> DNA
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<400> 330
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<210> 331
 <211> 2168
 <212> DNA
 <213> Homo Sapien

<400> 331
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 gtgtgagatg tttcagtgaa ccaaagttct gataccttgt ttacatgttt 2100

gtttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys	35	40	45	
Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser	50	55	60	
Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp	65	70	75	
Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val	80	85	90	
Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu	95	100	105	
Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg	110	115	120	
Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala	125	130	135	
Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile	140	145	150	
Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser	155	160	165	
Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly	170	175	180	
Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln	185	190	195	
Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu	200	205	210	

Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Phe	Gln	Leu	Gly	Asp	Leu	His	Arg	215	220	225
Ala	Leu	Glu	Leu	Thr	Arg	Arg	Leu	Leu	Ser	Leu	Asp	Pro	Ser	His	230	235	240
Glu	Arg	Ala	Gly	Gly	Asn	Leu	Arg	Tyr	Phe	Glu	Gln	Leu	Leu	Glu	245	250	255
Glu	Glu	Arg	Glu	Lys	Thr	Leu	Thr	Asn	Gln	Thr	Glu	Ala	Glu	Leu	260	265	270
Ala	Thr	Pro	Glu	Gly	Ile	Tyr	Glu	Arg	Pro	Val	Asp	Tyr	Leu	Pro	275	280	285
Glu	Arg	Asp	Val	Tyr	Glu	Ser	Leu	Cys	Arg	Gly	Glu	Gly	Val	Lys	290	295	300
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Gly	Asn	Arg	Ala	Pro	Gln	Leu	Leu	Ile	Ala	Pro	Phe	Lys	Glu	Glu	320	325	330
Asp	Glu	Trp	Asp	Ser	Pro	His	Ile	Val	Arg	Tyr	Tyr	Asp	Val	Met	335	340	345
Ser	Asp	Glu	Glu	Ile	Glu	Arg	Ile	Lys	Glu	Ile	Ala	Lys	Pro	Lys	350	355	360
Leu	Ala	Arg	Ala	Thr	Val	Arg	Asp	Pro	Lys	Thr	Gly	Val	Leu	Thr	365	370	375
Val	Ala	Ser	Tyr	Arg	Val	Ser	Lys	Ser	Ser	Trp	Leu	Glu	Glu	Asp	380	385	390
Asp	Asp	Pro	Val	Val	Ala	Arg	Val	Asn	Arg	Arg	Met	Gln	His	Ile	395	400	405
Thr	Gly	Leu	Thr	Val	Lys	Thr	Ala	Glu	Leu	Leu	Gln	Val	Ala	Asn	410	415	420
Tyr	Gly	Val	Gly	Gly	Gln	Tyr	Glu	Pro	His	Phe	Asp	Phe	Ser	Arg	425	430	435
Arg	Pro	Phe	Asp	Ser	Gly	Leu	Lys	Thr	Glu	Gly	Asn	Arg	Leu	Ala	440	445	450
Thr	Phe	Leu	Asn	Tyr	Met	Ser	Asp	Val	Glu	Ala	Gly	Gly	Ala	Thr	455	460	465
Val	Phe	Pro	Asp	Leu	Gly	Ala	Ala	Ile	Trp	Pro	Lys	Lys	Gly	Thr	470	475	480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
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Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
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<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

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Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
				35					40					45
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
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Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
				65					70					75
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
				80					85					90
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala

	95		100		105									
Val	Leu	Thr	Ser	Arg	Ala	Thr	Leu	Ser	Thr	Leu	Ala	Val	Ala	Val
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Asn	Arg	Thr	Val	Ala	His	His	Phe	Pro	Arg	Leu	Leu	Tyr	Phe	Thr
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Gly	Gln	Arg	Gly	Ala	Arg	Ala	Pro	Ala	Gly	Met	Gln	Val	Val	Ser
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His	Gly	Asp	Glu	Arg	Pro	Ala	Trp	Leu	Met	Ser	Glu	Thr	Leu	Arg
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Glu	Glu	Phe	Ile	Gly	Ala	Gly	Glu	Gln	Ala	Arg	Tyr	Cys	His	Gly
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Cys	Val	Ser	Gln	His	Gln	Gly	Gln	Gln	Tyr	Arg	Ser	Phe	Glu	Leu
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Ala	Lys	Asn	Arg	Asp	Pro	Glu	Lys	Glu	Gly	Ser	Ser	Ala	Phe	Leu
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Ser	Ala	Phe	Ala	Val	His	Pro	Val	Ser	Glu	Gly	Thr	Leu	Met	Tyr
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Arg	Leu	His	Lys	Arg	Phe	Ser	Ala	Leu	Glu	Leu	Glu	Arg	Ala	Tyr
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Ser	Glu	Ile	Glu	Gln	Leu	Gln	Ala	Gln	Ile	Arg	Asn	Leu	Thr	Val
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Leu	Thr	Pro	Glu	Gly	Glu	Ala	Gly	Leu	Ser	Trp	Pro	Val	Gly	Leu
				350					355					360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp		365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala		380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp		395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro		410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg		425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu		440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg		455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met		470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu		485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe		500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu		515	520	525
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Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg		545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala		560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro		575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly		590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp		605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu		620	625	630

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Asn	Ala	Asp	Tyr	Leu	Ala	Ala	Arg	Ala	Arg	Leu	Ala	Gly	Glu	Leu
				680					685					690
Ala	Gly	Gln	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Glu	Val	Met
				695					700					705
Asp	Val	Phe	Leu	Arg	Phe	Ser	Gly	Leu	His	Leu	Phe	Arg	Ala	Val
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Glu	Pro	Gly	Leu	Val	Gln	Lys	Phe	Ser	Leu	Arg	Asp	Cys	Ser	Pro
				725					730					735
Arg	Leu	Ser	Glu	Glu	Leu	Tyr	His	Arg	Cys	Arg	Leu	Ser	Asn	Leu
				740					745					750
Glu	Gly	Leu	Gly	Gly	Arg	Ala	Gln	Leu	Ala	Met	Ala	Leu	Phe	Glu
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<212> DNA

<213> Homo Sapien

<400> 340

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<212> PRT

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Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	35	40	45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg	50	55	60	
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Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	80	85	90	
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Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	110	115	120	
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Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile	140	145	150	
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Met His Val Met	Met Tyr Gly Val Tyr	Arg Leu Arg Ala Phe	Gly		
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<210> 344

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<210> 348

<211> 48

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<210> 349

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<400> 356
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<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro	50	55	60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser	65	70	75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser	80	85	90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu	95	100	105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser	110	115	120	
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg	125	130	135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp	140	145	150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp	155	160	165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala	170	175	180	

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
 185 190 195

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Asn Pro Leu Asn Lys Gly Lys Ser Leu
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cagaaggatg tcccgtggaa 20

<210> 391

<211> 17

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gccgctgtcc actgcag 17

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atgtcctcca tgcccacgcg 20

<210> 394

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caggccccct tgatctgtac ccca 24

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gccaggcctc acattcgt 18

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<400> 421

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<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

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<211> 310

<212> PRT

<213> Homo Sapien

<400> 423

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Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu	35	40	45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr	50	55	60	
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Lys	Ile	Gln	Asp	Glu	Gln	Thr	65	70	75	
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly	80	85	90	
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Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	110	115	120	
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Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val	140	145	150	
Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Glu	Gly	155	160	165	
His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu	170	175	180	
Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe	185	190	195	

His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His
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Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala
				215					220					225
Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
				230					235					240
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
				245					250					255
Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
				260					265					270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
				275					280					285
Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly
				290					295					300
Asp	Phe	Arg	His	Lys	Ser	Ser	Phe	Val	Ile					
				305					310					